

Supplemental Table S1: Strain phenotypes.

| Strain | 15mM Caffeine 1 | 15mM Caffeine 2 | 1M NaCl 1 | 1M NaCl 2 |
|--------------|--------------------|--------------------|-----------|-----------|
| 273614X_b | 1.29 | 1.27 | 0.41 | 0.52 |
| CBS2888_1b | 1.77 | 1.66 | 0.28 | 0.41 |
| CBS3093_1b | 1.69 | 1.82 | 0.18 | 0.32 |
| CBS7960_2 | 0.76 | 0.78 | 0.91 | 0.90 |
| CECT10109_1b | 0.51 | 0.60 | 0.89 | 1.07 |
| CECT10266_1b | 0.81 | 1.19 | 0.94 | 1.16 |
| CEN.PK | 0.38 | 0.39 | 0.06 | 0.06 |
| CLIB154_1b | 0.43 | 0.42 | 0.96 | 0.96 |
| CLIB219_2b | 0.51 | 0.41 | 0.13 | 0.09 |
| CLIB272_2 | 0.75 | 0.82 | 1.31 | 1.83 |
| CLIB274_1 | 0.93 | 1.21 | 0.19 | 0.42 |
| CLIB294_1b | 0.81 | 0.52 | 1.11 | 0.77 |
| CLIB318_1 | 0.30 | 0.37 | 1.67 | 1.48 |
| CLIB324_2 | 0.75 | 0.67 | 0.84 | 0.72 |
| CLIB326_1 | 0.64 | 0.30 | 0.66 | 0.30 |
| CLIB382_1b | 0.50 | 0.40 | 1.01 | 0.90 |
| CLIB413_1b | 0.82 | 0.57 | 1.48 | 1.00 |
| DBVPG1339_1b | 0.23 | 0.25 | 1.27 | 1.01 |
| DBVPG1788_1b | 0.97 | 0.70 | 1.78 | 1.33 |
| DBVPG1794_1b | 0.75 | 0.57 | 1.78 | 1.30 |
| DBVPG3591_1b | 0.48 | 0.44 | 1.05 | 0.99 |
| DBVPG4651_1b | 0.45 | 0.45 | 0.37 | 0.32 |
| DBVPG6861 | 0.46 | 0.44 | 0.83 | 0.85 |
| EM93_3 | 0.54 | 0.49 | 0.78 | 0.74 |
| FL200 | 0.75 | 0.77 | 0.77 | 0.70 |
| FY5 | 0.62 | 0.66 | 1.09 | 1.21 |
| I14_1b | 0.70 | 0.77 | 1.30 | 1.37 |
| IL_01_b | 0.42 | 0.44 | 1.24 | 1.21 |
| K1_1 | 0.20 | 0.19 | 0.83 | 0.97 |
| K12_2 | 0.75 | 0.69 | 0.68 | 0.58 |
| M22_1b | 1.59 | 2.31 | 2.33 | 2.69 |
| NC_02_b | 1.36 | 1.27 | 0.07 | 0.07 |
| PW5_b | 0.44 | 0.45 | 0.05 | 0.05 |
| RM11_1b | 0.55 | 0.62 | 0.90 | 0.98 |
| Sigma | 1.23 | 1.03 | 0.14 | 0.15 |
| SK1208 | 0.53 | 0.27 | 0.16 | 0.11 |
| T7_b | 1.19 | 1.15 | 0.38 | 0.37 |
| T73_1b | 0.72 | 0.73 | 1.08 | 1.07 |
| UC1_1b | 1.40 | 1.35 | 1.08 | 0.98 |
| UC8_1b | 0.67 | 0.65 | 1.23 | 1.21 |
| WE372_1b | 0.65 | 0.61 | 1.25 | 1.09 |
| Y10_1b | 0.08 | 0.08 | 0.25 | 0.21 |
| Y12_b | 0.62 | 0.64 | 0.90 | 0.85 |
| Y3_1b | 1.33 | 0.89 | 0.18 | 0.68 |
| Y55_1b | 1.39 | 1.20 | 2.91 | 0.51 |

| | | | | |
|------------|------|------|------|------|
| Y9_4 | 0.47 | 0.43 | 0.99 | 0.89 |
| Y9J_1b | 0.99 | 1.02 | 0.51 | 0.60 |
| YJM145_b | 0.79 | 0.82 | 0.46 | 0.50 |
| YJM269_1b | 0.51 | 0.53 | 1.26 | 1.29 |
| YJM280_b | 0.34 | 0.42 | 0.42 | 0.35 |
| YJM320_b | 0.48 | 0.52 | 0.67 | 0.66 |
| YJM326_b | 2.04 | 2.17 | 0.51 | 0.60 |
| YJM413_b | 1.13 | 1.13 | 0.29 | 0.23 |
| YJM421_1b | 0.90 | 0.78 | 0.54 | 0.58 |
| YJM428_1b | 0.79 | 0.92 | 0.65 | 0.77 |
| YJM434_1b | 0.88 | 0.78 | 1.12 | 1.01 |
| YJM436_1b | 0.44 | 0.45 | 1.17 | 1.15 |
| YJM440_1b | 1.63 | 1.54 | 0.75 | 0.78 |
| YJM454_1b | 1.19 | 1.19 | 0.15 | 0.25 |
| YJM653_1b | 0.27 | 0.12 | 0.95 | 0.99 |
| YJM678_1b | 1.25 | 1.38 | 0.33 | 0.19 |
| YJM981_b | 0.52 | 0.70 | 1.39 | 1.74 |
| YPS1000_1b | 0.90 | 0.91 | 0.56 | 0.23 |
| YPS1009_b | 1.19 | 1.15 | 0.28 | 0.20 |
| YPS163_1b | 1.12 | 1.10 | 0.50 | 0.26 |

Each measurement is the average growth of four technical replicates adjusted for growth on YPD alone. The average of the two biological replicates is plotted in Figure 2A. Strains used in the round-robin cross are indicated in red.

Supplemental Table S2: Summary of RR segregant data and corresponding QTL patterns.

| Cross | MATx | MATa | Segregants Salt | Epistasis test Salt | Salt QTL alleles | Segregants Caffeine | Epistasis test Caffeine | Caffeine QTL alleles |
|-------|---------|---------|-------------------------|------------------------|--------------------------------------|------------------------|-------------------------------|-------------------------------------|
| 1 | YPS1009 | I14 | Complex (negative) | 5.65E-07 | Complex (1 from each strain) | Complex (negative) | 0.006 | Complex (3 YPS1009, 1 I14) |
| 2 | Y10 | I14 | Bimodal | 0.313 | Bimodal (only ENA from I14) | Transgressive | 0.981 | Complex (5 I14 alleles) |
| 3 | Y10 | PW5 | Slight transgressive | 0.880 | Complex (2 from each strain) | Transgressive | 0.875 | Complex (1 Y10, 4 PW5) |
| 4 | PW5 | 273614X | Complex | 0.775 | Complex (1 PW5, 8 273614x) | Transgressive | 0.021 | Complex (1 from each) |
| 5 | YJM981 | 273614X | Bimodal | 0.367 | Complex (2 from each strain) | Complex | 0.866 | Complex (4 YJM981, 2 273614x) |
| 6 | YJM981 | CBS2888 | Complex (negative) | 6.72E-05 | Complex (4 YJM981, 1 CBS2888) | Complex | 1.000 | Complex (1 YJM981, 4 CBS2888) |
| 7 | CLIB219 | CBS2888 | ND | 0.775 | Complex (5 CLIB219, 8 CBS2888) | Nearly Bimodal | 0.299 | Bimodal (1 CBS2888) |
| 8 | M22 | CLIB219 | Transgressive | 0.917 | Complex (5 M22, 3 CLIB219) | Transgressive | 0.608 | Complex (1 M22, 4 CLIB219) |
| 9 | YJM269 | M22 | Transgressive | 0.859 | Complex (3 YJM269) | Transgressive | 0.997 | Complex (1 YJM269, 2 M22) |
| 10 | NC-02 | YJM269 | Complex (negative) | 0.602 | Complex (2 NC-02, 5 YJM269) | Transgressive | 0.970 | Complex (4 NC-02, 3 YJM269) |
| 11 | NC-02 | YJM454 | ND | 0.880 | Complex (4 NC-02, 5 YJM454) | Unimodal | 0.857 | Bimodal (1 YJM454) |
| 12 | YPS1009 | YJM454 | ND | 0.300 | Complex (1 YPS1009, 8 YJM454) | Unimodal | 0.291 | None |

Significant Epistasis scores

Supplemental Table S3: Replicate confirmed BY/RM QTL.

| QTL | Condition | Chromo-some | LOD score | Max LOD position | Lower bound of QTL | Upper bound of QTL | Replicate Pairs |
|--------------|------------------|--------------------|------------------|-------------------------|---------------------------|---------------------------|------------------------|
| Caff.chr01.1 | 15mM Caffeine | chr01 | 6.83 | 34500 | 16450 | 52550 | 4 |
| Caff.chr04.1 | 15mM Caffeine | chr04 | 6.25 | 371625 | 335950 | 411600 | 4 |
| Caff.chr04.2 | 15mM Caffeine | chr04 | 8.75 | 594125 | 565375 | 624725 | 4 |
| Caff.chr08.1 | 15mM Caffeine | chr08 | 13.51 | 174625 | 159825 | 190750 | 4 |
| Caff.chr11.1 | 15mM Caffeine | chr11 | 50.85 | 57675 | 52375 | 63675 | 4 |
| Caff.chr12.1 | 15mM Caffeine | chr12 | 7.75 | 470275 | 446450 | 498700 | 4 |
| Caff.chr13.1 | 15mM Caffeine | chr13 | 20.31 | 245500 | 233500 | 278525 | 4 |
| Caff.chr14.1 | 15mM Caffeine | chr14 | 55.88 | 472725 | 463975 | 481850 | 4 |
| Caff.chr15.1 | 15mM Caffeine | chr15 | 7.01 | 74875 | 48325 | 102050 | 4 |
| Caff.chr15.2 | 15mM Caffeine | chr15 | 22.97 | 625325 | 615775 | 636200 | 4 |
| NaCl.chr09.1 | 1M NaCl | chr09 | 7.06 | 117700 | 86525 | 153525 | 4 |
| NaCl.chr14.1 | 0.5M & 1M NaCl | chr14 | 19.32 | 376000 | 359675 | 388975 | 6 |

QTL that passed a LOD score threshold of 5 and were identified in at least one pair of technical replicates are listed.

Supplemental Table S4: Grouped RR QTL

| Condition | QTL | Chromosome | LOD score | Max LOD position | Lower bound of QTL | Upper bound of QTL | Crosses with QTL | # Crosses with QTL | Number of Coding Variants in QTL | Significant Variants | Association Score Coding Variants | Association Score All Variants | Candidate OTG |
|-----------|--------------|------------|-----------|------------------|--------------------|--------------------|--------------------------|--------------------|----------------------------------|----------------------|-----------------------------------|--------------------------------|-------------------|
| Caffeine | Caff.chr03.1 | chr03 | 8.22 | 288775 | 267550 | 291500 | 8 | 1 | 109 | 13 | 0.535 | 0.535 | |
| | Caff.chr04.1 | chr04 | 6.06 | 463300 | 442650 | 502800 | 1 | 1 | 155 | 13 | 0.628 | 0.628 | |
| | Caff.chr04.2 | chr04 | 38.12 | 877925 | 866200 | 896475 | 2,3 | 2 | 48 | 4 | 0.999 | 0.999 | MSS4 |
| | Caff.chr07.1 | chr07 | 8.04 | 513400 | 468500 | 567450 | 2,3 | 2 | 221 | 28 | 0.762 | 0.762 | MSB2,MTL1,GSC2 |
| | Caff.chr08.1 | chr08 | 14.76 | 25675 | 18175 | 41725 | 5 | 1 | 83 | 7 | 0.507 | 0.507 | GUT1,VMR1 |
| | Caff.chr08.2 | chr08 | 8.53 | 178850 | 133700 | 207650 | 10 | 1 | 221 | 23 | 0.517 | 0.517 | SLT2 |
| | Caff.chr09.1 | chr09 | 5.58 | 412900 | 397400 | 413000 | 5 | 1 | 60 | 2 | 0.992 | 0.992 | |
| | Caff.chr10.1 | chr10 | 29.08 | 561025 | 547725 | 569800 | 1,2,3,5,6,8,9,10 | 8 | 77 | 4 | 0.349 | 0.356 | TOR1 (confirmed) |
| | Caff.chr10.2 | chr10 | 28.77 | 459000 | 431300 | 477200 | 5,6 | 2 | 112 | 3 | 0.793 | 0.793 | CYR1 |
| | Caff.chr11.1 | chr11 | 10.81 | 59650 | 46400 | 73900 | 1,2,3,6,11 | 5 | 79 | 2 | 0.320 | 0.371 | TOR2 |
| | Caff.chr11.2 | chr11 | 7.23 | 633650 | 613500 | 634000 | 4,5 | 2 | 70 | 3 | 0.690 | 0.690 | |
| | Caff.chr12.1 | chr12 | 9.44 | 653850 | 614300 | 682850 | 9 | 1 | 183 | 15 | 0.501 | 0.501 | HAP1,GSY2 |
| | Caff.chr12.2 | chr12 | 6.90 | 460250 | 446550 | 484850 | 10 | 1 | 5 | 0 | 0.128 | 0.794 | |
| | Caff.chr13.1 | chr13 | 10.07 | 26975 | 14900 | 51250 | 10 | 1 | 124 | 12 | 0.315 | 0.445 | RSC9,ATR1,GTR1 |
| | Caff.chr14.1 | chr14 | 5.65 | 227800 | 207250 | 276150 | 1 | 1 | 232 | 12 | 0.320 | 0.617 | |
| | Caff.chr14.2 | chr14 | 19.63 | 468650 | 453125 | 482700 | 10 | 1 | 96 | 10 | 0.426 | 0.535 | |
| | Caff.chr15.1 | chr15 | 8.61 | 625275 | 604100 | 648050 | 2,4,9,10 | 4 | 139 | 2 | 0.413 | 0.413 | PDR5 |
| | Caff.chr15.2 | chr15 | 8.42 | 45200 | 40650 | 49150 | 3 | 1 | 32 | 2 | 0.291 | 0.506 | |
| | Caff.chr15.3 | chr15 | 38.56 | 406200 | 395000 | 421500 | 5,7,8 | 3 | 107 | 8 | 0.778 | 0.778 | WHI2 (confirmed) |
| | Caff.chr15.4 | chr15 | 8.94 | 136725 | 115125 | 163375 | 6 | 1 | 166 | 17 | 0.409 | 0.409 | WSC3,PKH2 |
| | Caff.chr15.5 | chr15 | 7.44 | 1005250 | 978600 | 1033900 | 10 | 1 | 175 | 13 | 0.358 | 0.502 | |
| | Caff.chr16.1 | chr16 | 21.14 | 416875 | 389900 | 435400 | 6,8 | 2 | 130 | 8 | 0.428 | 0.996 | BRO1,RGL1 |
| | Caff.chr16.2 | chr16 | 6.85 | 208000 | 187200 | 236800 | 8 | 1 | 209 | 8 | 0.777 | 0.777 | TC089 |
| NaCl | NaCl.chr02.1 | chr02 | 11.84 | 538250 | 510450 | 567050 | 10,11,12 | 3 | 203 | 5 | 0.841 | 0.841 | IRA1 |
| | NaCl.chr02.2 | chr02 | 6.47 | 238950 | 189950 | 269050 | 11 | 1 | 227 | 12 | 0.483 | 0.483 | |
| | NaCl.chr03.1 | chr03 | 5.62 | 33600 | 14900 | 54750 | 7 | 1 | 111 | 0 | 0.243 | 0.360 | |
| | NaCl.chr03.2 | chr03 | 6.55 | 289800 | 263700 | 291500 | 8 | 1 | 124 | 5 | 0.351 | 0.351 | |
| | NaCl.chr04.1 | chr04 | 41.24 | 509600 | 491650 | 531850 | 1,2,3,5,6,7,8,9,10,11,12 | 11 | 51 | 0 | 0.180 | 0.465 | ENA locus |
| | NaCl.chr04.2 | chr04 | 18.21 | 421750 | 411600 | 429050 | 3 | 1 | 48 | 1 | 0.235 | 0.574 | GPD1 |
| | NaCl.chr04.3 | chr04 | 6.05 | 192600 | 142400 | 230050 | 7 | 1 | 229 | 22 | 0.476 | 0.830 | |
| | NaCl.chr04.4 | chr04 | 9.00 | 834700 | 797100 | 861150 | 7 | 1 | 190 | 0 | 0.217 | 0.452 | |
| | NaCl.chr04.5 | chr04 | 6.55 | 1397800 | 1368600 | 1412700 | 7 | 1 | 113 | 13 | 0.538 | 0.538 | |
| | NaCl.chr05.1 | chr05 | 15.35 | 107825 | 81750 | 133825 | 4 | 1 | 162 | 0 | 0.454 | 0.454 | |
| | NaCl.chr05.2 | chr05 | 8.21 | 514325 | 493975 | 546450 | 4,7 | 2 | 168 | 0 | 0.306 | 0.471 | BCK2 |
| | NaCl.chr05.3 | chr05 | 9.87 | 418800 | 387600 | 441000 | 12 | 1 | 141 | 10 | 0.414 | 0.604 | SHO1 |
| | NaCl.chr07.1 | chr07 | 10.67 | 932050 | 898400 | 958400 | 4,5,7 | 3 | 195 | 14 | 0.504 | 0.504 | |
| | NaCl.chr07.2 | chr07 | 8.20 | 536050 | 511300 | 571500 | 4,6,11 | 3 | 104 | 5 | 0.406 | 0.406 | MSB2,MTL1,GSC2 |
| | NaCl.chr07.3 | chr07 | 6.20 | 15000 | 14900 | 22300 | 7 | 1 | 11 | 0 | 0.113 | 0.337 | |
| | NaCl.chr08.1 | chr08 | 13.02 | 51250 | 27250 | 65125 | 4,5,10 | 3 | 171 | 10 | 0.829 | 0.829 | GUT1,WSC4,VMR1 |
| | NaCl.chr10.1 | chr10 | 8.93 | 548300 | 530050 | 561300 | 3,4 | 2 | 108 | 10 | 0.727 | 0.727 | OSM1,STK2 |
| | NaCl.chr10.2 | chr10 | 28.50 | 434650 | 420250 | 451625 | 5,6 | 2 | 81 | 4 | 0.888 | 0.888 | CYR1 |
| | NaCl.chr10.3 | chr10 | 21.11 | 204725 | 182800 | 234375 | 6,10 | 2 | 143 | 2 | 0.476 | 0.476 | YJL107c & YJL108c |
| | NaCl.chr10.4 | chr10 | 6.09 | 104300 | 78050 | 150900 | 9 | 1 | 221 | 23 | 0.500 | 0.500 | |
| | NaCl.chr10.5 | chr10 | 6.52 | 37400 | 14900 | 53550 | 11 | 1 | 117 | 4 | 0.422 | 0.488 | |
| | NaCl.chr11.1 | chr11 | 12.84 | 66850 | 49425 | 78250 | 8,10,11 | 3 | 86 | 5 | 0.368 | 0.636 | TOR2 |
| | NaCl.chr11.2 | chr11 | 5.46 | 598050 | 542750 | 639900 | 9 | 1 | 355 | 13 | 0.484 | 0.494 | |
| | NaCl.chr11.3 | chr11 | 7.24 | 237750 | 206100 | 262650 | 10 | 1 | 204 | 8 | 0.563 | 0.606 | |
| | NaCl.chr12.1 | chr12 | 10.72 | 872550 | 854850 | 891450 | 7 | 1 | 99 | 0 | 0.430 | 0.465 | |
| | NaCl.chr12.2 | chr12 | 13.79 | 457350 | 428400 | 475850 | 12 | 1 | 84 | 10 | 0.671 | 0.671 | |
| | NaCl.chr13.1 | chr13 | 8.09 | 288300 | 255700 | 338200 | 3,4,12 | 3 | 252 | 2 | 0.689 | 0.689 | |
| | NaCl.chr13.2 | chr13 | 6.35 | 571100 | 532600 | 615800 | 4 | 1 | 314 | 17 | 0.406 | 0.409 | |
| | NaCl.chr13.3 | chr13 | 15.45 | 706900 | 671575 | 720300 | 7,11 | 2 | 216 | 12 | 0.420 | 0.420 | EFR3 |
| | NaCl.chr14.1 | chr14 | 8.01 | 582200 | 550350 | 605000 | 4,8,12 | 3 | 92 | 2 | 0.555 | 0.555 | CRZ1 |
| | NaCl.chr14.2 | chr14 | 6.28 | 139400 | 132300 | 145900 | 11 | 1 | 39 | 1 | 0.337 | 0.922 | |
| | NaCl.chr14.3 | chr14 | 10.61 | 263050 | 225900 | 299900 | 12 | 1 | 240 | 28 | 0.438 | 0.438 | |
| | NaCl.chr15.1 | chr15 | 21.98 | 73800 | 57650 | 87150 | 6,11,12 | 3 | 81 | 3 | 0.311 | 0.416 | YGK3 |
| | NaCl.chr15.2 | chr15 | 57.10 | 408100 | 398850 | 412700 | 7,8,12 | 3 | 64 | 4 | 0.939 | 0.939 | WHI2 (confirmed) |
| | NaCl.chr15.3 | chr15 | 9.67 | 1020100 | 992200 | 1042025 | 8,10 | 2 | 143 | 9 | 0.478 | 0.856 | PDE2 |
| | NaCl.chr16.1 | chr16 | 6.81 | 434250 | 399150 | 481050 | 1,7,8 | 3 | 213 | 0 | 0.628 | 0.628 | |
| | NaCl.chr16.2 | chr16 | 43.89 | 206950 | 200625 | 212175 | 7,8 | 2 | 47 | 6 | 0.922 | 0.922 | TCO89,RTT10 |

Legend

QTL Identifier
 Combined LOD score of grouped QTL
 Max LOD position
 Position with highest LOD score across grouped QTL
 Crosses with QTL
 Round-robin crosses in which the QTL was detected
 Lower/upper bound of QTL
 2-LOD confidence interval of QTL
 Number of Coding Variants in QTL
 Non-synonymous coding variants within the QTL interval across the RR parent strains
 Significant Variants
 Number of non-synonymous coding variants with a significant association score
 Association Score Coding Variants
 Maximum association score among non-synonymous coding variants
 Association Score All Variants
 Maximum association score among all variants within the QTL interval
 Candidate QTG Candidate quantitative trait genes based on Saccharomyces Genome Database gene annotations

Supplemental Table S5: GO Analyses

Salt resistance QTL**Function GO terms**GOID GO_term
16740 transferase activity

Cluster frequency 128 out of 851 genes, 15.0%
 Background frequency 741 out of 7167 background genes, 10.3%
 P-value 0.00113
 FDR 0
 Expected FP 0
 Gene(s) annotated to the term
 ALK2/YBL009W-SCT1/YBL011W-FMT1/YBL013W-FUS3/YBL016W-RER2/YBL002C-COO1/YBL003W-GPI18/YBL004C-MNN2/YBL015C-MEC1/YBL136W-BMT2/YBL141C-CSH1/YBL161W-GLK1/YBL040W-APA1/YBL05C-PBN1/YBL052C-SPB1/YBL054W-KIN82/YCR091W-NOP1/YDL014W-CDC7/YDL017W-LYS21/YDL131W-RP021/YDL140C-CRD1/YDL142C-RPC5/YDL150W-STE7/YDL159W-AIR2/YDL175C-ARO3/YDL035W-ARG82/YDL173C-NGG1/YDL176W-SAS4/YDL181C-CAB5/YDL196C-RKM2/YDL198C-PAF5/YDL459C-RMT2/YDL465C-PKH3/YDL466W-SDC1/YDL469W-SNE1/YDL477W-GLC3/YDL11W-BUD16/YEL029C-YCK3/YER123W-SAK1/YER129W-GCG1/YER163C-CCA1/YER168C-ADK2/YER170W-TMT1/YER175C-NMA2/YGR010W-UGA1/YGR019W-THG1/YGR024C-GSC2/YGR032W-PMT6/YGR199W-PCT1/YGR202C-CCH1/YGR203W-SL1/YGR212W-GPI1/YGR216C-DIE2/YGR227W-GUT1/YHL032C-OST1/YL0102C-CTK2/YL006C-IME2/YL106W-GCD14/YL125C-SP10/YL127C-YAK1/YL141C-RPA34/YL148W-TPK1/YL164C-HAL5/YL165C-ERG20/YL167W-SET2/YL168C-MNN1/YL183W-MNN5/YL186W-SWE1/YL187C-YL218W-POL31/YR006W-CDC8/YJR057W-YR066W-HSL1/YR066W-HSL1/YR066W-HSL1/YR066W-HSL1/YR066W-HSL1/YR066W-HSL1/WCDC5/YMR001C-SEC59/YMR013C-RIM11/YMR139W-PFK2/YMR205C-ERG12/YMR208W-SKY1/YMR216C-ERG8/YMR220W-MRE11/YMR224C-ARK1/YNL020C-RCM1/YNL022C-RCM2/YNL024C-KTR5/YNL029C-GPI15/YNL038W-NPR1/YNL183C-DUG3/YNL191W-CHS1/YNL192W-RIO2/YNL207W-ALG9/YNL139W-PFK2/YMR205C-ERG12/YMR208W-SKY1/YMR216C-ERG8/YMR220W-MRE11/YMR224C-ARK1/YNL020C-RCM1/YNL022C-RCM2/YNL024C-KTR5/YNL029C-GPI15/YNL038W-NPR1/YNL183C-DUG3/YNL191W-CHS1/WCDC5/YMR001C-SEC59/YMR013C-RIM11/YMR139W-PFK2/YMR205C-ERG12/YMR208W-SKY1/YMR216C-ARK1/YNL020C-NPR1/YNL183C-RIO2/YNL207W-PIK1/YNL257W-YGK3/YOL128C-GAS4/YOL132W-PFK27/YOL136C-ARG8/YOL140W-PPM2/YOL141W-GFA1/YK1104C-AAT1/YK1106W-PRR1/YK1116C-YPK1/YK1126W-PTK1/YL163C-ERG20/YK1204W-TRM2/YK1205W-GLG1/YK1206W-KTR2/YK1206W-GPT2/YK1206W-MET1/YK1206W-ECM4/YK1207W-TGL4/YK1209C-PEP4/YK1209C-SUR4/YL1372W-TRM12/YM1005W-CDCS/YMR001C-SEC59/YMR013C-RIM11/YMR139W-SWPI1/YMR149W-PFK2/YMR205C-ERG12/YMR208W-YMR209C-YMR210W-GAS3/YMR215W-SKY1/YMR216C-ERG8/YMR220W-MRE11/YMR224C-ARK1/YNL020C-RCM1/YNL022C-RCM2/YNL024C-KTR5/YNL029C-GPI15/YNL038W-NPR1/YNL183C-DUG3/YNL191W-CHS1/YNL192W-RIO2/YNL207W-ALG9/YNL139W-PFK2/YMR205C-ERG12/YMR208W-SKY1/YMR216C-ERG8/YMR220W-MRE11/YMR224C-ARK1/YNL020C-RCM1/YNL022C-RCM2/YNL024C-KTR5/YNL029C-GPI15/YNL038W-NPR1/YNL183C-DUG3/YNL191W-CHS1/WCDC5/YMR001C-SEC59/YMR013C-RIM11/YMR139W-PFK2/YMR205C-ERG12/YMR208W-SKY1/YMR216C-ARK1/YNL020C-NPR1/YNL183C-RIO2/YNL207W-PIK1/YNL257W-YGK3/YOL128C-3C:SUR1/YPL057C-BTS1/YPL069C-GP12/YPL076W

16301 kinase activity

46 out of 851 genes, 5.4%
 200 out of 7167 background genes, 2.8%
 P-value 0.00205
 FDR 0
 Expected FP 0
 Gene(s) annotated to the term
 ALK2/YBL009W-FUS3/YBL016W-MEC1/YBL136W-GLK1/YBL040W-KIN82/YCR091W-CDC7/YDL159W-ARG82/YD173C-CAB5/YDL196C-PKH3/YDL466W-SNF1/YDL477W-BUD16/YEL029C-YCK3/YER123W-SAK1/YER129W-ADK2/YER170W-GU1/YHL032C-CTK2/YL006C-IME2/YL106W-YAK1/YL141C-TPK1/YL164C-HAL5/YL165C-SWE1/YL187C-CDC8/YOL057W-PTK2/YJ059W-TOR1/YJ066W-HSL1/YK101W-PR1/YK116C-TPK1/YK126W-PTK1/YK198C-TOR2/YK1203C-CD55/YMR001C-SEC59/YMR013C-RIM11/YMR139W-PFK2/YMR205C-ERG12/YMR208W-SKY1/YMR216C-ERG8/YMR220W-MRE11/YMR224C-ARK1/YNL020C-RCM1/YNL022C-RCM2/YNL024C-KTR5/YNL029C-GPI15/YNL038W-NPR1/YNL183C-DUG3/YNL191W-CHS1/YNL192W-RIO2/YNL207W-ALG9/YNL139W-PFK2/YMR205C-ERG12/YMR208W-SKY1/YMR216C-ARK1/YNL020C-NPR1/YNL183C-RIO2/YNL207W-PIK1/YNL257W-YGK3/YOL128C-3C:UPR1/YPL057C-BTS1/YPL069C-GP12/YPL076W

16773 phosphotransferase activity, alcohol group as acceptor

42 out of 851 genes, 4.9%
 178 out of 7167 background genes, 2.5%
 P-value 0.00266
 FDR 0
 Expected FP 0
 Gene(s) annotated to the term
 ALK2/YBL009W-FUS3/YBL016W-MEC1/YBL136W-GLK1/YBL040W-KIN82/YCR091W-CDC7/YDL159W-ARG82/YD173C-CAB5/YDL196C-PKH3/YDL466W-SNF1/YDL477W-BUD16/YEL029C-YCK3/YER123W-SAK1/YER129W-ADK2/YER170W-GU1/YHL032C-CTK2/YL006C-IME2/YL106W-YAK1/YL141C-TPK1/YL164C-HAL5/YL165C-SWE1/YL187C-CDC8/YOL057W-PTK2/YJ059W-TOR1/YJ066W-HSL1/YK101W-PR1/YK116C-TPK1/YK126W-PTK1/YK198C-TOR2/YK1203C-CD55/YMR001C-SEC59/YMR013C-RIM11/YMR139W-PFK2/YMR205C-ERG12/YMR208W-SKY1/YMR216C-ERG8/YMR220W-MRE11/YMR224C-ARK1/YNL020C-RCM1/YNL022C-RCM2/YNL024C-KTR5/YNL029C-GPI15/YNL038W-NPR1/YNL183C-DUG3/YNL191W-CHS1/YNL192W-RIO2/YNL207W-ALG9/YNL139W-PFK2/YMR205C-ERG12/YMR208W-SKY1/YMR216C-ARK1/YNL020C-NPR1/YNL183C-RIO2/YNL207W-PIK1/YNL257W-YGK3/YOL128C-3C:UPR1/YPL057C-BTS1/YPL069C-GP12/YPL076W

4672 protein kinase activity

32 out of 851 genes, 3.8%
 132 out of 7167 background genes, 1.8%
 P-value 0.01849
 FDR 0
 Expected FP 0
 Gene(s) annotated to the term
 ALK2/YBL009W-FUS3/YBL016W-MEC1/YBL136W-GLK1/YBL040W-KIN82/YCR091W-CDC7/YDL159W-PK18/YDR466W-SNF1/YDL477W-BUD16/YEL029C-YCK3/YER123W-SAK1/YER129W-ADK2/YER170W-GU1/YHL032C-CTK2/YL006C-IME2/YL106W-YAK1/YL141C-TPK1/YL164C-HAL5/YL165C-SWE1/YL187C-CDC8/YOL057W-PTK2/YJ059W-TOR1/YJ066W-HSL1/YK101W-PR1/YK116C-TPK1/YK126W-PTK1/YK198C-TOR2/YK1203C-CD55/YMR001C-SEC59/YMR013C-RIM11/YMR139W-SKY1/YMR216C-ARK1/YNL020C-NPR1/YNL183C-RIO2/YNL207W-PIK1/YNL257W-YGK3/YOL128C-3C:UPR1/YPL057C-BTS1/YPL069C-GP12/YPL076W

16758 transferase activity, transferring hexosyl groups

22 out of 851 genes, 2.6%
 80 out of 7167 background genes, 1.1%
 P-value 0.03874
 FDR 0
 Expected FP 0
 Gene(s) annotated to the term
 GP18/YBL004C-MNN2/YBL015C-CSH1/YBL161W-PBN1/YCL052C-GLC3/YEL011W-GSC2/YGR032W-PMT6/YGR199W-GPI1/YGR216C-DIE2/YGR227W-OST1/YL002C-MNN11/YL183W-MNN5/YL186W-GLG1/YK058W-KTR2/YK061W-SWP1/YMR149W-KTR5/YNL029C-GPI15/YNL038W-CSH1/YNL192W-ALG9/YNL192C-MNN9/YPL050C-SUR1/YPL057C-GP12/YPL076W

Process GO termsGOID GO_term
51716 cellular response to stimulus

Cluster frequency 134 out of 851 genes, 15.7%
 Background frequency 788 out of 7167 background genes, 11.0%
 P-value 0.00614
 FDR 0
 Expected FP 0
 Gene(s) annotated to the term
 PDR3/YBL009W-FUS3/YBL016W-UGA2/YBL006W-HHT1/YBL010W-GRX7/YBL014C-MEC1/YBL136W-RA1/YBL140C-KAR4/YCL052C-ADP1/YCL055W-PPM1/YCL058C-ADP1/YCL059W-PPM1/YCL060C-ADP1/YCL061W-PPM1/YCL062C-ADP1/YCL063W-PPM1/YCL064C-ADP1/YCL065W-PPM1/YCL066C-ADP1/YCL067W-PPM1/YCL068C-ADP1/YCL069W-PPM1/YCL070C-ADP1/YCL071W-PPM1/YCL072C-ADP1/YCL073W-PPM1/YCL074C-ADP1/YCL075W-PPM1/YCL076C-ADP1/YCL077W-PPM1/YCL078C-ADP1/YCL079W-PPM1/YCL080C-ADP1/YCL081W-PPM1/YCL082C-ADP1/YCL083W-PPM1/YCL084C-ADP1/YCL085W-PPM1/YCL086C-ADP1/YCL087W-PPM1/YCL088C-ADP1/YCL089W-PPM1/YCL090C-ADP1/YCL091W-PPM1/YCL092C-ADP1/YCL093W-PPM1/YCL094C-ADP1/YCL095W-PPM1/YCL096C-ADP1/YCL097W-PPM1/YCL098C-ADP1/YCL099W-PPM1/YCL100C-ADP1/YCL101W-PPM1/YCL102C-ADP1/YCL103W-PPM1/YCL104C-ADP1/YCL105W-PPM1/YCL106C-ADP1/YCL107W-PPM1/YCL108C-ADP1/YCL109W-PPM1/YCL110C-ADP1/YCL111W-PPM1/YCL112C-ADP1/YCL113W-PPM1/YCL114C-ADP1/YCL115W-PPM1/YCL116C-ADP1/YCL117W-PPM1/YCL118C-ADP1/YCL119W-PPM1/YCL120C-ADP1/YCL121W-PPM1/YCL122C-ADP1/YCL123W-PPM1/YCL124C-ADP1/YCL125W-PPM1/YCL126C-ADP1/YCL127W-PPM1/YCL128C-ADP1/YCL129W-PPM1/YCL130C-ADP1/YCL131W-PPM1/YCL132C-ADP1/YCL133W-PPM1/YCL134C-ADP1/YCL135W-PPM1/YCL136C-ADP1/YCL137W-PPM1/YCL138C-ADP1/YCL139W-PPM1/YCL140C-ADP1/YCL141W-PPM1/YCL142C-ADP1/YCL143W-PPM1/YCL144C-ADP1/YCL145W-PPM1/YCL146C-ADP1/YCL147W-PPM1/YCL148C-ADP1/YCL149W-PPM1/YCL150C-ADP1/YCL151W-PPM1/YCL152C-ADP1/YCL153W-PPM1/YCL154C-ADP1/YCL155W-PPM1/YCL156C-ADP1/YCL157W-PPM1/YCL158C-ADP1/YCL159W-PPM1/YCL160C-ADP1/YCL161W-PPM1/YCL162C-ADP1/YCL163W-PPM1/YCL164C-ADP1/YCL165W-PPM1/YCL166C-ADP1/YCL167W-PPM1/YCL168C-ADP1/YCL169W-PPM1/YCL170C-ADP1/YCL171W-PPM1/YCL172C-ADP1/YCL173W-PPM1/YCL174C-ADP1/YCL175W-PPM1/YCL176C-ADP1/YCL177W-PPM1/YCL178C-ADP1/YCL179W-PPM1/YCL180C-ADP1/YCL181W-PPM1/YCL182C-ADP1/YCL183W-PPM1/YCL184C-ADP1/YCL185W-PPM1/YCL186C-ADP1/YCL187W-PPM1/YCL188C-ADP1/YCL189W-PPM1/YCL190C-ADP1/YCL191W-PPM1/YCL192C-ADP1/YCL193W-PPM1/YCL194C-ADP1/YCL195W-PPM1/YCL196C-ADP1/YCL197W-PPM1/YCL198C-ADP1/YCL199W-PPM1/YCL200C-ADP1/YCL201W-PPM1/YCL202C-ADP1/YCL203W-PPM1/YCL204C-ADP1/YCL205W-PPM1/YCL206C-ADP1/YCL207W-PPM1/YCL208C-ADP1/YCL209W-PPM1/YCL210C-ADP1/YCL211W-PPM1/YCL212C-ADP1/YCL213W-PPM1/YCL214C-ADP1/YCL215W-PPM1/YCL216C-ADP1/YCL217W-PPM1/YCL218C-ADP1/YCL219W-PPM1/YCL220C-ADP1/YCL221W-PPM1/YCL222C-ADP1/YCL223W-PPM1/YCL224C-ADP1/YCL225W-PPM1/YCL226C-ADP1/YCL227W-PPM1/YCL228C-ADP1/YCL229W-PPM1/YCL230C-ADP1/YCL231W-PPM1/YCL232C-ADP1/YCL233W-PPM1/YCL234C-ADP1/YCL235W-PPM1/YCL236C-ADP1/YCL237W-PPM1/YCL238C-ADP1/YCL239W-PPM1/YCL240C-ADP1/YCL241W-PPM1/YCL242C-ADP1/YCL243W-PPM1/YCL244C-ADP1/YCL245W-PPM1/YCL246C-ADP1/YCL247W-PPM1/YCL248C-ADP1/YCL249W-PPM1/YCL250C-ADP1/YCL251W-PPM1/YCL252C-ADP1/YCL253W-PPM1/YCL254C-ADP1/YCL255W-PPM1/YCL256C-ADP1/YCL257W-PPM1/YCL258C-ADP1/YCL259W-PPM1/YCL260C-ADP1/YCL261W-PPM1/YCL262C-ADP1/YCL263W-PPM1/YCL264C-ADP1/YCL265W-PPM1/YCL266C-ADP1/YCL267W-PPM1/YCL268C-ADP1/YCL269W-PPM1/YCL270C-ADP1/YCL271W-PPM1/YCL272C-ADP1/YCL273W-PPM1/YCL274C-ADP1/YCL275W-PPM1/YCL276C-ADP1/YCL277W-PPM1/YCL278C-ADP1/YCL279W-PPM1/YCL280C-ADP1/YCL281W-PPM1/YCL282C-ADP1/YCL283W-PPM1/YCL284C-ADP1/YCL285W-PPM1/YCL286C-ADP1/YCL287W-PPM1/YCL288C-ADP1/YCL289W-PPM1/YCL290C-ADP1/YCL291W-PPM1/YCL292C-ADP1/YCL293W-PPM1/YCL294C-ADP1/YCL295W-PPM1/YCL296C-ADP1/YCL297W-PPM1/YCL298C-ADP1/YCL299W-PPM1/YCL300C-ADP1/YCL301W-PPM1/YCL302C-ADP1/YCL303W-PPM1/YCL304C-ADP1/YCL305W-PPM1/YCL306C-ADP1/YCL307W-PPM1/YCL308C-ADP1/YCL309W-PPM1/YCL310C-ADP1/YCL311W-PPM1/YCL312C-ADP1/YCL313W-PPM1/YCL314C-ADP1/YCL315W-PPM1/YCL316C-ADP1/YCL317W-PPM1/YCL318C-ADP1/YCL319W-PPM1/YCL320C-ADP1/YCL321W-PPM1/YCL322C-ADP1/YCL323W-PPM1/YCL324C-ADP1/YCL325W-PPM1/YCL326C-ADP1/YCL327W-PPM1/YCL328C-ADP1/YCL329W-PPM1/YCL330C-ADP1/YCL331W-PPM1/YCL332C-ADP1/YCL333W-PPM1/YCL334C-ADP1/YCL335W-PPM1/YCL336C-ADP1/YCL337W-PPM1/YCL338C-ADP1/YCL339W-PPM1/YCL340C-ADP1/YCL341W-PPM1/YCL342C-ADP1/YCL343W-PPM1/YCL344C-ADP1/YCL345W-PPM1/YCL346C-ADP1/YCL347W-PPM1/YCL348C-ADP1/YCL349W-PPM1/YCL350C-ADP1/YCL351W-PPM1/YCL352C-ADP1/YCL353W-PPM1/YCL354C-ADP1/YCL355W-PPM1/YCL356C-ADP1/YCL357W-PPM1/YCL358C-ADP1/YCL359W-PPM1/YCL360C-ADP1/YCL361W-PPM1/YCL362C-ADP1/YCL363W-PPM1/YCL364C-ADP1/YCL365W-PPM1/YCL366C-ADP1/YCL367W-PPM1/YCL368C-ADP1/YCL369W-PPM1/YCL370C-ADP1/YCL371W-PPM1/YCL372C-ADP1/YCL373W-PPM1/YCL374C-ADP1/YCL375W-PPM1/YCL376C-ADP1/YCL377W-PPM1/YCL378C-ADP1/YCL379W-PPM1/YCL380C-ADP1/YCL381W-PPM1/YCL382C-ADP1/YCL383W-PPM1/YCL384C-ADP1/YCL385W-PPM1/YCL386C-ADP1/YCL387W-PPM1/YCL388C-ADP1/YCL389W-PPM1/YCL390C-ADP1/YCL391W-PPM1/YCL392C-ADP1/YCL393W-PPM1/YCL394C-ADP1/YCL395W-PPM1/YCL396C-ADP1/YCL397W-PPM1/YCL398C-ADP1/YCL399W-PPM1/YCL400C-ADP1/YCL401W-PPM1/YCL402C-ADP1/YCL403W-PPM1/YCL404C-ADP1/YCL405W-PPM1/YCL406C-ADP1/YCL407W-PPM1/YCL408C-ADP1/YCL409W-PPM1/YCL410C-ADP1/YCL411W-PPM1/YCL412C-ADP1/YCL413W-PPM1/YCL414C-ADP1/YCL415W-PPM1/YCL416C-ADP1/YCL417W-PPM1/YCL418C-ADP1/YCL419W-PPM1/YCL420C-ADP1/YCL421W-PPM1/YCL422C-ADP1/YCL423W-PPM1/YCL424C-ADP1/YCL425W-PPM1/YCL426C-ADP1/YCL427W-PPM1/YCL428C-ADP1/YCL429W-PPM1/YCL430C-ADP1/YCL431W-PPM1/YCL432C-ADP1/YCL433W-PPM1/YCL434C-ADP1/YCL435W-PPM1/YCL436C-ADP1/YCL437W-PPM1/YCL438C-ADP1/YCL439W-PPM1/YCL440C-ADP1/YCL441W-PPM1/YCL442C-ADP1/YCL443W-PPM1/YCL444C-ADP1/YCL445W-PPM1/YCL446C-ADP1/YCL447W-PPM1/YCL448C-ADP1/YCL449W-PPM1/YCL450C-ADP1/YCL451W-PPM1/YCL452C-ADP1/YCL453W-PPM1/YCL454C-ADP1/YCL455W-PPM1/YCL456C-ADP1/YCL457W-PPM1/YCL458C-ADP1/YCL459W-PPM1/YCL460C-ADP1/YCL461W-PPM1/YCL462C-ADP1/YCL463W-PPM1/YCL464C-ADP1/YCL465W-PPM1/YCL466C-ADP1/YCL467W-PPM1/YCL468C-ADP1/YCL469W-PPM1/YCL470C-ADP1/YCL471W-PPM1/YCL472C-ADP1/YCL473W-PPM1/YCL474C-ADP1/YCL475W-PPM1/YCL476C-ADP1/YCL477W-PPM1/YCL478C-ADP1/YCL479W-PPM1/YCL480C-ADP1/YCL481W-PPM1/YCL482C-ADP1/YCL483W-PPM1/YCL484C-ADP1/YCL485W-PPM1/YCL486C-ADP1/YCL487W-PPM1/YCL488C-ADP1/YCL489W-PPM1/YCL490C-ADP1/YCL491W-PPM1/YCL492C-ADP1/YCL493W-PPM1/YCL494C-ADP1/YCL495W-PPM1/YCL496C-ADP1/YCL497W-PPM1/YCL498C-ADP1/YCL499W-PPM1/YCL500C-ADP1/YCL501W-PPM1/YCL502C-ADP1/YCL503W-PPM1/YCL504C-ADP1/YCL505W-PPM1/YCL506C-ADP1/YCL507W-PPM1/YCL508C-ADP1/YCL509W-PPM1/YCL510C-ADP1/YCL511W-PPM1/YCL512C-ADP1/YCL513W-PPM1/YCL514C-ADP1/YCL515W-PPM1/YCL516C-ADP1/YCL517W-PPM1/YCL518C-ADP1/YCL519W-PPM1/YCL520C-ADP1/YCL521W-PPM1/YCL522C-ADP1/YCL523W-PPM1/YCL524C-ADP1/YCL525W-PPM1/YCL526C-ADP1/YCL527W-PPM1/YCL528C-ADP1/YCL529W-PPM1/YCL530C-ADP1/YCL531W-PPM1/YCL532C-ADP1/YCL533W-PPM1/YCL534C-ADP1/YCL535W-PPM1/YCL536C-ADP1/YCL537W-PPM1/YCL538C-ADP1/YCL539W-PPM1/YCL540C-ADP1/YCL541W-PPM1/YCL542C-ADP1/YCL543W-PPM1/YCL544C-ADP1/YCL545W-PPM1/YCL546C-ADP1/YCL547W-PPM1/YCL548C-ADP1/YCL549W-PPM1/YCL550C-ADP1/YCL551W-PPM1/YCL552C-ADP1/YCL553W-PPM1/YCL554C-ADP1/YCL555W-PPM1/YCL556C-ADP1/YCL557W-PPM1/YCL558C-ADP1/YCL559W-PPM1/YCL560C-ADP1/YCL561W-PPM1/YCL562C-ADP1/YCL563W-PPM1/YCL564C-ADP1/YCL565W-PPM1/YCL566C-ADP1/YCL567W-PPM1/YCL568C-ADP1/YCL569W-PPM1/YCL570C-ADP1/YCL571W-PPM1/YCL572C-ADP1/YCL573W-PPM1/YCL574C-ADP1/YCL575W-PPM1/YCL576C-ADP1/YCL577W-PPM1/YCL578C-ADP1/YCL579W-PPM1/YCL580C-ADP1/YCL581W-PPM1/YCL582C-ADP1/YCL583W-PPM1/YCL584C-ADP1/YCL585W-PPM1/YCL586C-ADP1/YCL587W-PPM1/YCL588C-ADP1/YCL589W-PPM1/YCL590C-ADP1/YCL591W-PPM1/YCL592C-ADP1/YCL593W-PPM1/YCL594C-ADP1/YCL595W-PPM1/YCL596C-ADP1/YCL597W-PPM1/YCL598C-ADP1/YCL599W-PPM1/YCL600C-ADP1/YCL601W-PPM1/YCL602C-ADP1/YCL603W-PPM1/YCL604C-ADP1/YCL605W-PPM1/YCL606C-ADP1/YCL607W-PPM1/YCL608C-ADP1/YCL609W-PPM1/YCL610C-ADP1/YCL611W-PPM1/YCL612C-ADP1/YCL613W-PPM1/YCL614C-ADP1/YCL615W-PPM1/YCL616C-ADP1/YCL617W-PPM1/YCL618C-ADP1/YCL619W-PPM1/YCL620C-ADP1/YCL621W-PPM1/YCL622C-ADP1/YCL623W-PPM1/YCL624C-ADP1/YCL625W-PPM1/YCL626C-ADP1/YCL627W-PPM1/YCL628C-ADP1/YCL629W-PPM1/YCL630C-ADP1/YCL631W-PPM1/YCL632C-ADP1/YCL633W-PPM1/YCL634C-ADP1/YCL635W-PPM1/YCL636C-ADP1/YCL637W-PPM1/YCL638C-ADP1/YCL639W-PPM1/YCL640C-ADP1/YCL641W-PPM1/YCL642C-ADP1/YCL643W-PPM1/YCL644C-ADP1/YCL645W-PPM1/YCL646C-ADP1/YCL647W-PPM1/YCL648C-ADP1/YCL649W-PPM1/YCL650C-ADP1/YCL651W-PPM1/YCL652C-ADP1/YCL653W-PPM1/YCL654C-ADP1/YCL655W-PPM1/YCL656C-ADP1/YCL657W-PPM1/YCL658C-ADP1/YCL659W-PPM1/YCL660C-ADP1/YCL661W-PPM1/YCL662C-ADP1/YCL663W-PPM1/YCL664C-ADP1/YCL665W-PPM1/YCL666C-ADP1/YCL667W-PPM1/YCL668C-ADP1/YCL669W-PPM1/YCL670C-ADP1/YCL671W-PPM1/YCL672C-ADP1/YCL673W-PPM1/YCL674C-ADP1/YCL675W-PPM1/YCL676C-ADP1/YCL677W-PPM1/YCL678C-ADP1/YCL679W-PPM1/YCL680C-ADP1/YCL681W-PPM1/YCL682C-ADP1/YCL683W-PPM1/YCL684C-ADP1/YCL685W-PPM1/YCL686C-ADP1/YCL687W-PPM1/YCL688C-ADP1/YCL689W-PPM1/YCL690C-ADP1/YCL691W-PPM1/YCL692C-ADP1/YCL693W-PPM1/YCL694C-ADP1/YCL695W-PPM1/YCL696C-ADP1/YCL697W-PPM1/YCL698C-ADP1/YCL699W-PPM1/YCL700C-ADP1/YCL701W-PPM1/YCL702C-ADP1/YCL703W-PPM1/YCL704C-ADP1/YCL705W-PPM1/YCL706C-ADP1/YCL707W-PPM1/YCL708C-ADP1/YCL709W-PPM1/YCL710C-ADP1/YCL711W-PPM1/YCL712C-ADP1/YCL713W-PPM1/YCL714C-ADP1/YCL715W-PPM1/YCL716C-ADP1/YCL717W-PPM1/YCL718C-ADP1/YCL719W-PPM1/YCL720C-ADP1/YCL721W-PPM1/YCL722C-ADP1/YCL723W-PPM1/YCL724C-ADP1/YCL725W-PPM1/YCL726C-ADP1/YCL727W-PPM1/YCL728C-ADP1/YCL729W-PPM1/YCL730C-ADP1/YCL731W-PPM1/YCL732C-ADP1/YCL733W-PPM1/YCL734C-ADP1/YCL735W-PPM1/YCL736C

| GOID | GO_term | Cluster frequency | Background frequency | P-value | FDR | Expected FP | Gene(s) annotated to the term |
|-------|----------------------|----------------------------|---|---------|------|-------------|--|
| 50896 | response to stimulus | 89 out of 461 genes, 19.3% | 941 out of 7167 background genes, 13.1% | 0.07729 | 0.04 | 0.04 | FIG2/YCR089W:KIN82/YCR091W:MSH13/YCR092C:CDC39/YCR093W:NHP10/YD002C:MC01/YD003W:RAD57/YD004W:SOK1/YD006C:GAL3/YD009W:SNQ2/YD011W:PSF1/YD013W:REG1/YD028C:RAD28/YD030C:UME6/YD0207C:UPC2/YD213W:AH1/YD214W:ADR1/YD216W:PDRI/YGL013C:SWC4/YGR002C:STF2/YGR008C:MSB2/YGR014W:MTL1/YGR023W:ERV1/YGR029W:ORM1/YGR038W:SBP1/YHL034C:VMR1/YHL035C:YHP9/YHR029C:SL7/YHR030C:SRB2/YHR041C:YHK8/YHR048W:DAL81/YIR023W:YH1/YIR026C:SAG1/YJR004C:POL31/YJR006W:CBF1/YJR060W:TOR1/YJR066W:RBC2/YJR068W:MNN4/YKL201C:TOR2/YKL203C:PC1/YKR095W:A:FAJ10/YLR238W:IRC20/YLR247C:RCK2/YLR248W:HAPI/YLR256W:LCBS/YLR260W:NE11/YLR265C:PD8R/YLR266C:ATR1/YML16W:GTR1/YML121W:RSC9/YML127W:EOS1/YNL080C:PM51/YNL082W:MK11/YNL085W:RH02/YNL090W:NST1/YNL091W:PSY2/YNL201C:RAP1/YNL216W:MGS1/YNL218W:ATG4/YNL223W:URE2/YNL229C:PRD16/YNL231C:MHF1/YOL086W:A:HAL9/YOL089C:MSH2/YOL090W:RFC4/YOL094C:PKH2/YOL100W:WSC3/YOL105C:SPT20/YOL148C:CKB2/YOR039W:WH12/YO434W:STD1/YOR047C:ELG1/YOR144C:PRD5/YOR153W:YR1/YOR162C:REV1/YOR346W:SG2/YOR353C:HAS5/YOR358W:PDE2/YOR360C:PIP2/YOR363C:RAD17/YOR368W:MRS6/YOR370C:GPB1/YOR371C:ALD6/YPL061W:GCR1/YPL075W:BRO1/YPL084W:REV3/YPL167C:TCO89/YPL180W:MF(ALPHA)1/YPL187W:PO55/YPL188W |

Supplemental Table S6: Copy number of *ENA* variants in the round-robin parent strains.

| Strain | chrIV coverage | ENA2 coverage | ENA2 copy number | ENA6 coverage | ENA6 copy number |
|---------------|---------------------------|--------------------------|-----------------------------|--------------------------|-----------------------------|
| YPS1009 | 70 | 0 | 0.00 | 6 | 0.09 |
| I14 | 73 | 173 | 2.37 | 20 | 0.27 |
| Y10 | 216 | 2 | 0.01 | 214 | 0.99 |
| PW5 | 421 | 3 | 0.01 | 382 | 0.91 |
| 273614x | 182 | 348 | 1.91 | 4 | 0.02 |
| YJM981 | 173 | 1007.5 | 5.82 | 76 | 0.44 |
| CBS2888 | 31 | 2 | 0.06 | 24 | 0.77 |
| Clib219 | 143 | 1 | 0.01 | 103 | 0.72 |
| M22 | 41 | 68 | 1.66 | 1 | 0.02 |
| YJM269 | 120 | 197 | 1.64 | 2 | 0.02 |
| NC-02 | 61 | 3 | 0.05 | 47 | 0.77 |
| YJM454 | 179 | 2 | 0.01 | 142 | 0.79 |

For each strain, sequences were aligned to the coding sequence of *ENA2* (Sacharomyces Genome Database S288c YDR039c) or *ENA6* (GenBank: FJ228230.1). In order to determine their copy number of the *ENA* variants, we calculated the median sequencing coverage of these two variants and compared it to the median coverage of chromosome IV, on which both genes are located.

Supplemental Table S7: Alleles underlying round-robin QTL.

Strain information

| Strain | Subgroup | Source |
|---------|-------------------|--|
| YPS1009 | Nature | Oak exudate, New Jersey, USA |
| I14 | Vineyard/Wine | Vineyard soil sample, Petrina, Italy |
| Y10 | Nature | From a coconut in the Phillipines |
| PW5 | Fermentation/Wine | Raphia Palm tree, Aba, Abia state, Nigeria |
| 273614x | Clinical isolate | Newcastle, UK |
| YJM981 | Clinical isolate | Bergamo, Italy |
| CBS2888 | Soil | South Africa |
| CLIB219 | Vineyard/Wine | Russia |
| M22 | Vineyard/Wine | Vineyard, Italy |
| YJM269 | Vineyard/Wine | From Blauer Portugieser grapes, Germany |
| NC-02 | Nature | Oak exudate, North Carolina, USA |
| YJM454 | Clinical isolate | USA |

Alleles identified for each grouped QTL

| QTL | Strains with beneficial alleles | Count | Strains with deleterious alleles | Count |
|--------------|--|-------|----------------------------------|-------|
| Caff.chr03.1 | CLIB219 | 1 | M22 | 1 |
| Caff.chr04.1 | YPS1009 | 1 | I14 | 1 |
| Caff.chr04.2 | I14,PW5 | 2 | Y10 | 1 |
| Caff.chr07.1 | I14,PW5 | 2 | Y10 | 1 |
| Caff.chr08.1 | YJM981 | 1 | 273614X | 1 |
| Caff.chr08.2 | NC-02 | 1 | YJM269 | 1 |
| Caff.chr09.1 | YJM981 | 1 | 273614X | 1 |
| Caff.chr10.1 | YPS1009,I14,PW5,273614X,CBS2888,CLIB219,YJM269,NC-02 | 8 | I14,Y10,YJM981,M22,YJM269 | 5 |
| Caff.chr10.2 | 273614X,CBS2888 | 2 | YJM981 | 1 |
| Caff.chr11.1 | I14,PW5,YJM981,YJM454 | 4 | YPS1009,Y10,CBS2888,NC-02 | 4 |
| Caff.chr11.2 | PW5,YJM981 | 2 | 273614X | 1 |
| Caff.chr12.1 | M22 | 1 | YJM269 | 1 |
| Caff.chr12.2 | YJM269 | 1 | NC-02 | 1 |
| Caff.chr13.1 | NC-02 | 1 | YJM269 | 1 |
| Caff.chr14.1 | YPS1009 | 1 | I14 | 1 |
| Caff.chr14.2 | YJM269 | 1 | NC-02 | 1 |
| Caff.chr15.1 | I14,273614X,M22,NC-02 | 4 | Y10,PW5,YJM269 | 3 |
| Caff.chr15.2 | Y10 | 1 | PW5 | 1 |
| Caff.chr15.3 | YJM981,CBS2888,M22 | 3 | 273614X,CLIB219 | 2 |
| Caff.chr15.4 | CBS2888 | 1 | YJM981 | 1 |
| Caff.chr15.5 | YJM269 | 1 | NC-02 | 1 |
| Caff.chr16.1 | CBS2888,CLIB219 | 2 | YJM981,M22 | 2 |
| Caff.chr16.2 | CLIB219 | 1 | M22 | 1 |
| NaCl.chr02.1 | NC-02,YPS1009 | 2 | YJM269,YJM454 | 2 |
| NaCl.chr02.2 | NC-02 | 1 | YJM454 | 1 |
| NaCl.chr03.1 | CBS2888 | 1 | CLIB219 | 1 |

| | | | | |
|--------------|--|---|---|---|
| NaCl.chr03.2 | CLIB219 | 1 | M22 | 1 |
| NaCl.chr04.1 | I14,PW5,YJM981,CLIB219,M22,YJM269,YJM454 | 7 | YPS1009,Y10,273614X,CBS2888,CLIB219,M22,NC-02 | 7 |
| NaCl.chr04.2 | PW5 | 1 | Y10 | 1 |
| NaCl.chr04.3 | CBS2888 | 1 | CLIB219 | 1 |
| NaCl.chr04.4 | CLIB219 | 1 | CBS2888 | 1 |
| NaCl.chr04.5 | CBS2888 | 1 | CLIB219 | 1 |
| NaCl.chr05.1 | 273614X | 1 | PW5 | 1 |
| NaCl.chr05.2 | 273614X,CBS2888 | 2 | PW5,CLIB219 | 2 |
| NaCl.chr05.3 | YJM454 | 1 | YPS1009 | 1 |
| NaCl.chr07.1 | 273614X,CBS2888 | 2 | PW5,YJM981,CLIB219 | 3 |
| NaCl.chr07.2 | 273614X,YJM981,NC-02 | 3 | PW5,CBS2888,YJM454 | 3 |
| NaCl.chr07.3 | CBS2888 | 1 | CLIB219 | 1 |
| NaCl.chr08.1 | PW5,YJM981,NC-02 | 3 | 273614X,YJM269 | 2 |
| NaCl.chr10.1 | Y10,273614X | 2 | PW5 | 1 |
| NaCl.chr10.2 | 273614X,CBS2888 | 2 | YJM981 | 1 |
| NaCl.chr10.3 | YJM981,YJM269 | 2 | CBS2888,NC-02 | 2 |
| NaCl.chr10.4 | YJM269 | 1 | M22 | 1 |
| NaCl.chr10.5 | YJM454 | 1 | NC-02 | 1 |
| NaCl.chr11.1 | M22,YJM269,YJM454 | 3 | CLIB219,NC-02 | 2 |
| NaCl.chr11.2 | YJM269 | 1 | M22 | 1 |
| NaCl.chr11.3 | YJM269 | 1 | NC-02 | 1 |
| NaCl.chr12.1 | CLIB219 | 1 | CBS2888 | 1 |
| NaCl.chr12.2 | YJM454 | 1 | YPS1009 | 1 |
| NaCl.chr13.1 | Y10,273614X,YJM454 | 3 | PW5,YPS1009 | 2 |
| NaCl.chr13.2 | 273614X | 1 | PW5 | 1 |
| NaCl.chr13.3 | CBS2888,NC-02 | 2 | CLIB219,YJM454 | 2 |
| NaCl.chr14.1 | 273614X,M22,YJM454 | 3 | PW5,CLIB219,YPS1009 | 3 |
| NaCl.chr14.2 | YJM454 | 1 | NC-02 | 1 |
| NaCl.chr14.3 | YJM454 | 1 | YPS1009 | 1 |
| NaCl.chr15.1 | YJM981,YJM454 | 2 | CBS2888,NC-02,YPS1009 | 3 |
| NaCl.chr15.2 | CBS2888,M22,YJM454 | 3 | CLIB219,YPS1009 | 2 |
| NaCl.chr15.3 | M22,YJM269 | 2 | CLIB219,NC-02 | 2 |
| NaCl.chr16.1 | YPS1009,CLIB219 | 2 | I14,CBS2888,M22 | 3 |
| NaCl.chr16.2 | CLIB219 | 1 | CBS2888,M22 | 2 |

For each instance of a QTL we determined whether each of the two strains involved in the corresponding cross contributed the beneficial or deleterious allele based on the allele frequency skews post selection.

Supplemental Table S8: Round-robin mating type dependent QTL.

| Cross | Condition | Chromosome | LOD score | Max LOD position | Lower bound of QTL | Upper bound of QTL | Candidate QTG |
|----------|---------------|------------|-----------|------------------|--------------------|--------------------|---------------|
| Cross 2 | YPD | chr12 | 8.8 | 1040100 | 1027900 | 1051000 | SST2 |
| Cross 2 | 1M NaCl | chr12 | 8.23 | 1041700 | 1026000 | 1050600 | SST2 |
| Cross 2 | 15mM Caffeine | chr12 | 6.27 | 1045100 | 1021500 | 1050600 | SST2 |
| Cross 2 | 20mM Caffeine | chr12 | 5.81 | 1049800 | 987900 | 1051000 | SST2 |
| Cross 3 | 0.5M NaCl | chr04 | 9.49 | 884100 | 855600 | 907000 | MSS4 |
| Cross 4 | 0.5M NaCl | chr12 | 12.3 | 18800 | 14900 | 25300 | |
| Cross 4 | 1M NaCl | chr04 | 6.89 | 364800 | 343300 | 392800 | |
| Cross 4 | 1M NaCl | chr12 | 6.58 | 15000 | 14900 | 31600 | |
| Cross 4 | 1M NaCl | chr15 | 9.14 | 420900 | 304500 | 443300 | |
| Cross 5 | YPD | chr08 | 6.12 | 109300 | 84300 | 140100 | GPA1 |
| Cross 5 | 1M NaCl | chr08 | 6.75 | 101300 | 14900 | 146400 | GPA1 |
| Cross 5 | 20mM Caffeine | chr08 | 7.43 | 108800 | 89400 | 140400 | GPA1 |
| Cross 8 | YPD | chr06 | 9.46 | 18200 | 14900 | 23300 | |
| Cross 8 | YPD | chr08 | 11.85 | 31100 | 19100 | 51800 | |
| Cross 8 | YPD | chr16 | 6.19 | 399000 | 377500 | 422700 | |
| Cross 8 | 15mM Caffeine | chr11 | 7.68 | 65400 | 54700 | 74200 | TOR2 |
| Cross 8 | 20mM Caffeine | chr11 | 7.04 | 62800 | 49800 | 72900 | TOR2 |
| Cross 9 | 20mM Caffeine | chr08 | 5.01 | 45100 | 14900 | 80600 | |
| Cross 10 | YPD | chr08 | 8.58 | 94200 | 80300 | 121900 | GPA1 |
| Cross 10 | 1M NaCl | chr08 | 5.87 | 105400 | 87000 | 120700 | GPA1 |
| Cross 10 | 15mM Caffeine | chr08 | 7.58 | 93900 | 83500 | 103900 | GPA1 |
| Cross 10 | 15mM Caffeine | chr13 | 5.62 | 41500 | 14900 | 78900 | |
| Cross 10 | 20mM Caffeine | chr08 | 5.67 | 94100 | 73300 | 122900 | GPA1 |
| Cross 10 | 20mM Caffeine | chr13 | 5.84 | 58900 | 14900 | 90200 | |
| Cross 11 | 0.5M NaCl | chr07 | 8.4 | 104900 | 63400 | 122400 | |

QTL identified in multiple conditions are indicated in green. We excluded the 1M sodium chloride (NaCl) selections for Cross 11 from this analysis as this selection was stringent for this cross and few cells grew under this condition. While comparison of the MAT α and MAT α selection experiments reproducibly identify QTL, QTL not shared between the two mating types are likely false positives resulting from the small number of segregants with in the mapping pool.